

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 107181834  
Source: IFUS  
Date Processed by STIC: 2-8-05

***ENTERED***



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/718,834

DATE: 02/08/2005

TIME: 12:26:49

Input Set : A:\Sequence Listing.ST25.txt  
 Output Set: N:\CRF4\02082005\J718834.raw

3 <110> APPLICANT: Wyeth  
 4 O'Toole, Margot  
 5 Mounts, William M  
 6 Shojaee, Negin  
 8 <120> TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING LUPUS NEPHRITIS  
 10 <130> FILE REFERENCE: 031896-091000  
 12 <140> CURRENT APPLICATION NUMBER: US 10/718,834  
 13 <141> CURRENT FILING DATE: 2003-11-21  
 15 <150> PRIOR APPLICATION NUMBER: US 60/428,065  
 16 <151> PRIOR FILING DATE: 2002-11-21  
 18 <160> NUMBER OF SEQ ID NOS: 21  
 20 <170> SOFTWARE: PatentIn version 3.3  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 3652  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Homo sapiens  
 27 <400> SEQUENCE: 1  
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 30 tcctccccgc atccagaaag tcccaggctg cccaaacctc tctgggacag agaaaaatt 120  
 32 ggcaagggtt aaggtcacca gcacattcag gatttctctc aaaagtccca tctccgtct 180  
 34 atttgtgg aatccagtga ggtgaatgaa gagagtgggg atctccattt gccccatgag 240  
 36 gagctgctgc tgctcaactga tggtgaggaa gaggatgctg aggcccttcc ccaagaccaa 300  
 38 agtgaagagc cagggcgcc acgtccccat catcaggctc ggcaagtgga gcattcgacg 360  
 40 cagcgcggcc atctggagat tcgggagctg aagaagaagc tgttcaaacg ccggcggtg 420  
 42 ttgaatcggg agcggcgtct gaggccaccgg gtggcgcccc ctgtataga ccaaggcg 480  
 44 atcacgcggc accaccta aagcgggc gctcaggagc tgtcccaaga aatcaaggct 540  
 46 ttctgtactg gcttagaccc cattctgggc caccaactct cagcccgga acatgctcgc 600  
 48 tgggtcttc tcctgtccg ttcttgcca cctgctcggg ctgctgtct tgaccacttg 660  
 50 agaggtgtct ttgatgagag tgccggcc cacctggctg ccctggatga aaccctgtg 720  
 52 gctggtccac ctcacccctcg tccaccccca ccctctcatg tccctgtgg tggacctgg 780  
 54 ctagaggatg tggttcagga agtgcagcag gtgctgtct agtttatccg ggccaaccca 840  
 56 aaggcctggg cacctgtat tagtgcattgg tccattgacc tcatgggca actgagcagc 900  
 58 acgtactcag gccagcacca gcgtgttccc cacgtactg ggcgtcttaa tgaactgcta 960  
 60 cagctgtgg agggttgttag gcccacgcgt acattaatgg acatctatgt gcagtgcctc 1020  
 62 tcggctctca ttggtagctg cccagatcgc tgggtggatg cttgtctgaa tacctctgtt 1080  
 64 cagcattctc cacacttga ctgggttgtg gcacatattg gtcctcttt tcctggcacc 1140  
 66 atcatttccc gggttctctc ctgtggcctt aaggacttt gtgtccatgg tggggctgg 1200  
 68 gttggagctg gcagtagtgg tggaaagctct tctcagaccc cctctacaga cccctccct 1260  
 70 gatctctgg ccattctgc ggagaaacgg gtgcccaaga ttgcctcaat tggatggatc 1320  
 72 ctaggtcacc tggcctcccg ccacggagat agcatccgac gggagctct gcgaatgttc 1380  
 74 catgatagcc tggcagggggg atctggaggc cgcaatggg accccctccct tcagccacg 1440  
 76 gttccgttcc tactgcagct ggcagtcatg tcaccagctt tgctggcac tgtctctgg 1500  
 78 gagttgtgg attgcctcaa gccccagct gtgctgagcc agctgcagca acaccccaa 1560

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82	gcctctgggg	caggtgccta	ccgcttgcgt	cagttcctgg	tggacacagc	tatgcctgct	1680											
84	tcggtcatta	ccaccagggg	cctggctgt	ccagacacccg	tgcgtgagc	ttgtgaccgg	1740											
86	ctaattccago	tgctgcgtct	gcacctgcaa	aaactggttc	atcacccggg	agggtctct	1800											
88	ggggaaagggg	tgcttaggccc	gcccccaccc	ccccgcttgg	tgccctttt	agatgcgctc	1860											
90	aaaaaccatg	ttggagagct	gtgtggagag	acgttacat	tggaaacggaa	gcgcttcctc	1920											
92	tggcagcacc	agctcttggg	cctgctgtct	gtctataccc	gcoctagctg	tggacctgag	1980											
94	gccttggggc	atctgcgtag	ccgagcccg	agccctgaag	agttgagtt	ggccacccag	2040											
96	ttatatgcag	ggctagtgg	cagcctctct	ggcctctgc	ccctggctt	ccgaagctgt	2100											
98	ctggctcggg	tgcgtgcagg	gacattacag	cctccctca	cggcccggtt	cctgcgcaac	2160											
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104	gaggaggaag	tagctgaagc	tgctgcctct	ctccctggcca	tttgcctt	tccttctgaa	2340											
106	gccttatccc	cctccagct	cctgggactg	gtaagggctg	gggtgcacccg	cttcttgc	2400											
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110	tctcagacat	ccccagctgg	gctcaaggt	gcccgtc	tgctgggtga	aggagccta	2520											
112	catcgaggca	acacagaact	tttgggtgg	caagtagatg	gggacaatga	gactctctca	2580											
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116	gtctgtccag	gtcctggagg	gatttggtca	gtttccatg	ctggagtcat	cggccgtggc	2700											
118	ttaaagccac	ccaagttgt	ccagtcacga	aatcagcagg	aagtgtatct	taacacccag	2760											
120	agcctcctca	gcctcctgg	tcactgtgc	agtccccag	ggggcactga	atgtggggaa	2820											
122	tgctgggggg	caccatctt	gagtccagag	gcagccaaag	cagtggcagt	gacccgtgt	2880											
124	gagagtgtgt	gtcccgtatgc	agctgggtca	gagctggct	ggccccccga	gaaacacgccc	2940											
126	cgggcccaccc	tggagccgg	tctccgcatt	ggccggcgct	tccgcgaaca	gcccctgc	3000											
128	tttgcgtgt	taaagctgg	agcagctgca	ccccccagccc	tgtgtactg	ttccgtgt	3060											
130	cttcgggggc	tgctggccgc	cctttgggc	cattgggaag	cctctcgcca	ccctgacacg	3120											
132	acccactccc	cctggcacct	ggaggcatcc	tgcacccct	tggctgtcat	ggctgaggga	3180											
134	agcctcctgc	ctccggccct	gggtaatatg	catgaagat	ttagccaaact	ggcaccttcc	3240											
136	gagggtgcgtc	tgctgtgtct	cagtgtctgg	ggtttctcc	gggagcatgg	gcccttgcct	3300											
138	cagaagttca	tcttccaatc	agagcggggt	cgcttcattc	gggacttctc	cagggagggt	3360											
140	ggaggtgagg	gtggacccca	tctggctgt	ctgcacagt	tcctccaccc	caacatcgac	3420											
142	cgccttagtc	ttttctctgg	ccgtttccag	gcacccatc	cgtccactct	ccttcgacag	3480											
144	gggacgtage	cttttcttgc	tctggaaagcc	cagggagggt	gagcagttag	agagggaaagg	3540											
146	gactaacgtg	ctccggaaagg	gtggagggtt	ctcttctaag	tccttggct	aaagagcgct	3600											
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152	<211>	LENGTH:	1162															
153	<212>	TYPE:	PRT															
154	<213>	ORGANISM:	Homo sapiens															
156	<400>	SEQUENCE:	2															
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159	1				5				10						15			
162	Asn	Ser	Pro	Gly	Ser	Ser	Gln	His	Pro	Glu	Ser	Pro	Arg	Leu	Pro	Asn		
163						20				25				30				
166	Pro	Leu	Trp	Asp	Arg	Gly	Lys	Ile	Gly	Lys	Val	Glu	Gly	His	Gln	His		
167							35			40				45				
170	Ile	Gln	Asp	Phe	Ser	Gln	Lys	Ser	His	Leu	Pro	Ser	Ile	Val	Val	Glu		
171							50			55				60				
174	Ser	Ser	Glu	Val	Asn	Glu	Glu	Ser	Gly	Asp	Leu	His	Leu	Pro	His	Glu		

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175	65	70	75	80	
178	Glu Leu Leu Leu Leu	Thr Asp Gly Glu	Glu Asp Ala Glu Ala	Phe	
179		85	90	95	
182	Phe Gln Asp Gln Ser	Glu Glu Pro Gly Ala Ala Arg	Pro His His Gln		
183		100	105	110	
186	Ala Arg Gln Val Glu His Ser	Thr Gln Arg Gly His	Leu Glu Ile Arg		
187		115	120	125	
190	Glu Leu Lys Lys Lys Leu	Phe Lys Arg Arg Arg	Val Leu Asn Arg Glu		
191		130	135	140	
194	Arg Arg Leu Arg His Arg	Val Val Gly Ala Val	Ile Asp Gln Gly Leu		
195	145	150	155	160	
198	Ile Thr Arg His His	Leu Lys Lys Arg Ala Ala Gln	Glu Leu Ser Gln		
199		165	170	175	
202	Glu Ile Lys Ala Phe	Leu Thr Gly Val Asp Pro	Ile Leu Gly His Gln		
203		180	185	190	
206	Leu Ser Ala Arg Glu His	Ala Arg Cys Gly	Leu Leu Leu Arg Ser		
207		195	200	205	
210	Leu Pro Pro Ala Arg Ala	Ala Val Leu Asp His	Leu Arg Gly Val Phe		
211	210	215	220		
214	Asp Glu Ser Val Arg Ala	His Leu Ala Ala	Leu Asp Glu Thr Pro Val		
215	225	230	235	240	
218	Ala Gly Pro Pro His	Leu Arg Pro Pro Pro	Ser His Val Pro Ala		
219		245	250	255	
222	Gly Gly Pro Gly Leu	Glu Asp Val Val	Gln Glu Val Gln Val Leu		
223		260	265	270	
226	Ser Glu Phe Ile Arg Ala	Asn Pro Lys Ala Trp	Ala Pro Val Ile Ser		
227		275	280	285	
230	Ala Trp Ser Ile Asp	Leu Met Gly Gln	Leu Ser Ser Thr Tyr Ser Gly		
231		290	295	300	
234	Gln His Gln Arg Val	Pro His Ala Thr Gly	Ala Leu Asn Glu Leu		
235	305	310	315	320	
238	Gln Leu Trp Met Gly	Cys Arg Ala Thr Arg	Thr Leu Met Asp Ile Tyr		
239		325	330	335	
242	Val Gln Cys Leu Ser	Ala Leu Ile Gly	Ser Cys Pro Asp Ala Cys Val		
243		340	345	350	
246	Asp Ala Leu Leu Asp	Thr Ser Val Gln His	Ser Pro His Phe Asp Trp		
247		355	360	365	
250	Val Val Ala His Ile	Gly Ser Ser Phe	Pro Gly Thr Ile Ile Ser Arg		
251		370	375	380	
254	Val Leu Ser Cys Gly	Leu Lys Asp Phe Cys	Val His Gly Gly Ala Gly		
255		385	390	395	400
258	Gly Gly Ala Gly Ser	Ser Ser Gly Gly	Ser Ser Gln Thr Pro Ser Thr		
259		405	410	415	
262	Asp Pro Phe Pro Gly	Ser Pro Ala Ile	Pro Ala Glu Lys Arg Val Pro		
263		420	425	430	
266	Lys Ile Ala Ser Val	Val Gly Ile	Leu Gly His Leu Ala Ser Arg His		
267		435	440	445	
270	Gly Asp Ser Ile Arg	Arg Glu Leu	Leu Arg Met Phe His Asp Ser Leu		
271		450	455	460	

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274 Ala Gly Gly Ser Gly Arg Ser Gly Asp Pro Ser Leu Gln Ala Thr  
275 465 470 475 480  
278 Val Pro Phe Leu Leu Gln Leu Ala Val Met Ser Pro Ala Leu Leu Gly  
279 485 490 495  
282 Thr Val Ser Gly Glu Leu Val Asp Cys Leu Lys Pro Pro Ala Val Leu  
283 500 505 510  
286 Ser Gln Leu Gln Gln His Leu Gln Gly Phe Pro Arg Glu Glu Leu Asp  
287 515 520 525  
290 Asn Met Leu Asn Leu Ala Val His Leu Val Ser Gln Ala Ser Gly Ala  
291 530 535 540  
294 Gly Ala Tyr Arg Leu Leu Gln Phe Leu Val Asp Thr Ala Met Pro Ala  
295 545 550 555 560  
298 Ser Val Ile Thr Thr Gln Gly Leu Ala Val Pro Asp Thr Val Arg Glu  
299 565 570 575  
302 Ala Cys Asp Arg Leu Ile Gln Leu Leu Leu His Leu Gln Lys Leu  
303 580 585 590  
306 Val His His Arg Gly Gly Ser Pro Gly Glu Gly Val Leu Gly Pro Pro  
307 595 600 605  
310 Pro Pro Pro Arg Leu Val Pro Phe Leu Asp Ala Leu Lys Asn His Val  
311 610 615 620  
314 Gly Glu Leu Cys Gly Glu Thr Leu Arg Leu Glu Arg Lys Arg Phe Leu  
315 625 630 635 640  
318 Trp Gln His Gln Leu Leu Gly Leu Leu Ser Val Tyr Thr Arg Pro Ser  
319 645 650 655  
322 Cys Gly Pro Glu Ala Leu Gly His Leu Leu Ser Arg Ala Arg Ser Pro  
323 660 665 670  
326 Glu Glu Leu Ser Leu Ala Thr Gln Leu Tyr Ala Gly Leu Val Val Ser  
327 675 680 685  
330 Leu Ser Gly Leu Leu Pro Leu Ala Phe Arg Ser Cys Leu Ala Arg Val  
331 690 695 700  
334 His Ala Gly Thr Leu Gln Pro Pro Phe Thr Ala Arg Phe Leu Arg Asn  
335 705 710 715 720  
338 Leu Ala Leu Leu Val Gly Trp Glu Gln Gln Gly Glu Gly Pro Ala  
339 725 730 735  
342 Ala Leu Gly Ala His Phe Gly Glu Ser Ala Ser Ala His Leu Ser Asp  
343 740 745 750  
346 Leu Ala Pro Leu Leu His Pro Glu Glu Glu Val Ala Glu Ala Ala  
347 755 760 765  
350 Ala Ser Leu Leu Ala Ile Cys Pro Phe Pro Ser Glu Ala Leu Ser Pro  
351 770 775 780  
354 Ser Gln Leu Leu Gly Leu Val Arg Ala Gly Val His Arg Phe Phe Ala  
355 785 790 795 800  
358 Ser Leu Arg Leu His Gly Pro Pro Gly Val Ala Ser Ala Cys Gln Leu  
359 805 810 815  
362 Leu Thr Arg Leu Ser Gln Thr Ser Pro Ala Gly Leu Lys Ala Val Leu  
363 820 825 830  
366 Gln Leu Leu Val Glu Gly Ala Leu His Arg Gly Asn Thr Glu Leu Phe  
367 835 840 845  
370 Gly Gly Gln Val Asp Gly Asp Asn Glu Thr Leu Ser Val Val Ser Ala

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371	850	855	860
374	Ser Leu Ala Ser Ala Ser	Leu Leu Asp Thr Asn Arg Arg His Thr Ala	
375	865	870	875
378	Ala Val Pro Gly Pro Gly Gly Ile Trp Ser Val Phe His Ala Gly Val		880
379	885	890	895
382	Ile Gly Arg Gly Leu Lys Pro Pro Lys Phe Val Gln Ser Arg Asn Gln		
383	900	905	910
386	Gln Glu Val Ile Tyr Asn Thr Gln Ser Leu Leu Ser Leu Leu Val His		
387	915	920	925
390	Cys Cys Ser Ala Pro Gly Gly Thr Glu Cys Gly Glu Cys Trp Gly Ala		
391	930	935	940
394	Pro Ile Leu Ser Pro Glu Ala Ala Lys Ala Val Ala Val Thr Leu Val		
395	945	950	955
398	Glu Ser Val Cys Pro Asp Ala Ala Gly Ala Glu Leu Ala Trp Pro Pro		960
399	965	970	975
402	Glu Glu His Ala Arg Ala Thr Val Glu Arg Asp Leu Arg Ile Gly Arg		
403	980	985	990
406	Arg Phe Arg Glu Gln Pro Leu Leu Phe Glu Leu Leu Lys Leu Val Ala		
407	995	1000	1005
410	Ala Ala Pro Pro Ala Leu Cys Tyr Cys Ser Val Leu Leu Arg Gly		
411	1010	1015	1020
414	Leu Leu Ala Ala Leu Leu Gly His Trp Glu Ala Ser Arg His Pro		
415	1025	1030	1035
418	Asp Thr Thr His Ser Pro Trp His Leu Glu Ala Ser Cys Thr Leu		
419	1040	1045	1050
422	Val Ala Val Met Ala Glu Gly Ser Leu Leu Pro Pro Ala Leu Gly		
423	1055	1060	1065
426	Asn Met His Glu Val Phe Ser Gln Leu Ala Pro Phe Glu Val Arg		
427	1070	1075	1080
430	Leu Leu Leu Leu Ser Val Trp Gly Phe Leu Arg Glu His Gly Pro		
431	1085	1090	1095
434	Leu Pro Gln Lys Phe Ile Phe Gln Ser Glu Arg Gly Arg Phe Ile		
435	1100	1105	1110
438	Arg Asp Phe Ser Arg Glu Gly Gly Gly Glu Gly Pro His Leu		
439	1115	1120	1125
442	Ala Val Leu His Ser Val Leu His Arg Asn Ile Asp Arg Leu Gly		
443	1130	1135	1140
446	Leu Phe Ser Gly Arg Phe Gln Ala Pro Ser Pro Ser Thr Leu Leu		
447	1145	1150	1155
450	Arg Gln Gly Thr		
451	1160		
454	<210> SEQ ID NO: 3		
455	<211> LENGTH: 1162		
456	<212> TYPE: PRT		
457	<213> ORGANISM: Artificial		
459	<220> FEATURE:		
460	<223> OTHER INFORMATION: A variant of the human BFLP1698 polypeptide		
462	<400> SEQUENCE: 3		
464	Met Ala Leu Val Pro Gly Arg Ser Lys Glu Asp Gly Leu Trp Thr Arg		

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10,11,12,13,14

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/718,834

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